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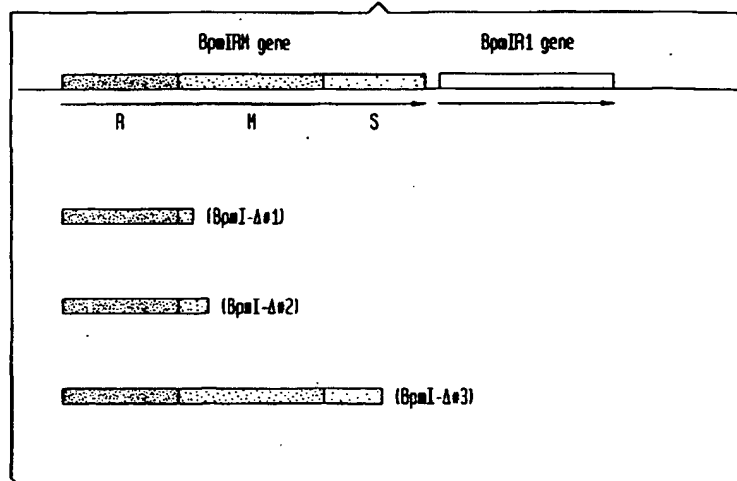
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(54) Method for cloning and expression of *BpmI* restriction endonuclease in *E. coli*

(57) The present invention relates to recombinant DNA which encodes the *BpmI* restriction endonuclease as well as *BpmI* methyltransferase, expression of *BpmI* restriction endonuclease from *E. coli* cells containing the recombinant DNA. *BpmI* endonuclease is a fusion of two distinct elements with a possible structural domains of restriction-methylationspecificity (R-M-S). This domain organization is analogous to the type I restriction-modification system with three distinct subunits, restriction,

methylation, and specificity (R, M, and S). Because *BpmI* is quite distinct to other type IIS restriction enzymes, it is proposed that *BpmI* belongs to a subgroup of type II restriction enzymes called type II<sub>f</sub> (f stands for fusion of restriction-modification-specificity domains). The Type II<sub>f</sub> group of restriction enzyme includes *Eco57I*, *BpmI*, *GsuI*, *BseRI* and some other restriction enzymes that cut downstream sequences at long distance, 10-20 bp downstream of recognition sequence, such as *MmeI* (N20/N18)).

FIG. 1



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## Description

**BACKGROUND OF THE INVENTION**

[0001] The present invention relates to recombinant DNA which encodes the *BpmI* restriction endonuclease as well as *BpmI* methyltransferase and expression of *BpmI* restriction endonuclease from *E. coli* cells containing the recombinant DNA. *BpmI* is an isoschizomer of *GsuI* (Fermentas 2000-2001 Catalog, Product No. ER0461/ER0462).

[0002] Type II restriction endonucleases are a class of enzymes that occur naturally in bacteria and in some viruses. When they are purified away from other bacterial proteins, restriction endonucleases can be used in the laboratory to cleave DNA molecules into small fragments for molecular cloning and gene characterization.

[0003] Restriction endonucleases act by recognizing and binding to particular sequences of nucleotides (the 'recognition sequence') along the DNA molecule. Once bound, they cleave the molecule within, to one side of, or to both sides of the recognition sequence. Different restriction endonucleases have affinity for different recognition sequences. Over two hundred and eleven restriction endonucleases with unique specificities have been identified among the many hundreds of bacterial species that have been examined to date (Roberts and Macelis, *Nucl. Acids Res.* 27:312-313 (1999)).

[0004] Restriction endonucleases typically are named according to the bacteria from which they are derived. Thus, the species *Deinococcus radiophilus* for example, produces three different restriction endonucleases, named *DraI*, *DraII* and *DraIII*. These enzymes recognize and cleave the sequences 5'TTT/AAA3', 5'PuG/GNCCPy3' and 5'CACNNN/GTG3' respectively. *Escherichia coli* RY13, on the other hand, produces only one enzyme, *EcoRI*, which recognizes the sequence 5'G/AATTC3'.

[0005] A second component of bacterial restriction-modification (R-M) systems are the methyltransferases (methylases). These enzymes are complementary to restriction endonucleases and they provide the means by which bacteria are able to protect their own DNA and distinguish it from foreign, infecting DNA. Modification methylases recognize and bind to the same recognition sequence as the corresponding restriction endonuclease, but instead of cleaving the DNA, they chemically modify one particular nucleotide within the sequence by the addition of a methyl group (C5-methyl cytosine, N4-methyl cytosine, or N6 methyl adenine). Following methylation, the recognition sequence is no longer cleaved by the cognate restriction endonuclease. The DNA of a bacterial cell is always fully modified by the activity of its modification methylase. It is therefore completely insensitive to the presence of the endogenous restriction endonuclease. It is only unmodified, and therefore identifiably foreign DNA, that is sensitive to restriction endonuclease recognition and cleavage.

[0006] By means of recombinant DNA technology, it is now possible to clone genes and overproduce the enzymes in large quantities. The key to isolating clones of restriction endonuclease genes is to develop a simple and reliable method to identify such clones within complex genomic DNA libraries, i.e. populations of clones derived by 'shotgun' procedures, when they occur at frequencies as low as  $10^{-3}$  to  $10^{-4}$ . Preferably, the method should be selective, such that the unwanted majority of clones are destroyed while the desirable rare clones survive.

[0007] A large number of type II restriction-modification systems have been cloned. The first cloning method used bacteriophage infection as a means of identifying or selecting restriction endonuclease clones (*EcoRII*: Kosykh et al., *Mol. Gen. Genet.* 178:717-719 (1980); *HhaI*: Mann et al., *Gene* 3:97-112 (1978); *PstI*: Walder et al., *Proc. Nat. Acad. Sci.* 78:1503-1507 (1981)). Since the presence of restriction-modification systems in bacteria enable them to resist infection by bacteriophage, cells that carry cloned restriction-modification genes can, in principle, be selectively isolated as survivors from genomic DNA libraries that have been exposed to phages. This method has been found, however, to have only limited value. Specifically, it has been found that cloned restriction-modification genes do not always manifest sufficient phage resistance to confer selective survival.

[0008] Another cloning approach involves transferring systems initially characterized as plasmid-borne into *E. coli* cloning plasmids (*EcoRV*: Bougueleret et al., *Nucl. Acids. Res.* 12:3659-3676 (1984); *PaeR7*: Gingeras and Brooks, *Proc. Natl. Acad. Sci. USA* 80:402-406 (1983); Theriault and Roy, *Gene* 19:355-359 (1982); *PvuII*: Blumenthal et al., *J. Bacteriol.* 164:501-509 (1985); *Tsp45I*: Wayne et al. *Gene* 202:83-88 (1997)).

[0009] A third approach is to select for active expression of methylase genes (methylase selection) (U.S. Patent No. 5,200,333 and *BsuRI*: Kiss et al., *Nucl. Acids. Res.* 13:6403-6421 (1985)). Since R-M genes are often closely linked together, both genes can often be cloned simultaneously. This selection does not always yield a complete restriction system however, but instead yields only the methylase gene (*BspRI*: Szomolanyi et al., *Gene* 10:219-225 (1980); *BcnI*: Janulaitis et al., *Gene* 20:197-204 (1982); *BsuRI*: Kiss and Baldauf, *Gene* 21:111-119 (1983); and *MspI*: Walder et al., *J. Biol. Chem.* 258:1235-1241 (1983)).

[0010] A more recent method, the "endo-blue method", has been described for direct cloning of restriction endonuclease genes in *E. coli* based on the indicator strain of *E. coli* containing the *dinD::lacZ* fusion (Fomenkov et al., U.S. Patent No. 5,498,535, (1996); Fomenkov et al., *Nucl. Acids Res.* 22:2399-2403 (1994)). This method utilizes the *E. coli* SOS response signals following DNA damages caused by restriction endonucleases or non-specific nucleases. A

number of thermostable nuclease genes (*TaqI*, *Tth1111*, *BsoBI*, *T7* nuclease) have been cloned by this method (U.S. Patent No. 5,498,535).

[0011] Because purified restriction endonucleases, and to a lesser extent, modification methylases, are useful tools for creating recombinant molecules in the laboratory, there is a commercial incentive to obtain bacterial strains through recombinant DNA techniques that produce large quantities of restriction enzymes. Such overexpression strains should also simplify the task of enzyme purification.

## SUMMARY OF THE INVENTION

[0012] The present invention relates to a method for cloning the *BpmI* restriction endonuclease from *Bacillus pumilus* into *E. coli* by methylase selection and inverse PCR amplification of the adjacent DNA of the *BpmI* methylase gene.

[0013] The present invention relates to recombinant *BpmI* and methods for producing the same. *BpmI* restriction endonuclease is found in the strain of *Bacillus pumilus* (New England Biolabs' strain collection #711). It recognizes doublestranded DNA sequence 5' CTGGAG 3' (or 5'CTCCAG3') and cleaves 16/14 bases downstream of its recognition sequence (N16/N14) to generate a 2-base 3' overhanging ends.

[0014] By methylase selection, a methylase gene with high homology to amino-methyltransferases (N6-adenine methylases) was found in a DNA library. This gene was named *BpmI* M1 gene (*BpmIM1*, 1650 bp), encoding a 549-aa protein with predicted molecular mass of 63,702 daltons. There was one partial open reading frame upstream of *BpmIM1* gene that displayed 31% amino acid sequence identity to another restriction enzyme *Eco57I* with similar recognition sequence (*Eco57I* recognition sequence: 5'CTGAAG N16/N14; *BpmI* recognition sequence: 5' CTGGAG N16/N14; A. Janulaitis et al. *Nucl. Acids Res.* 20:6051-6056, (1992)).

[0015] In order to clone the rest of the *BpmIRM* gene, inverse PCR was used to amplify the adjacent DNA sequence. After four rounds of inverse PCR reactions, an open reading frame of 3030 bp was found upstream of *BpmI* M1 methylase gene, which encodes a 1009-aa protein with predicted molecular mass of 116,891 daltons. By amino acid sequence comparison of *BpmI* endonuclease with all known proteins in GenBank protein database, it was discovered that *BpmI* endonuclease is a fusion of two distinct elements with a possible structural domains of restriction-methylation-specificity (R-M-S). This domain organization is analogous to the type I restriction-modification system with three distinct subunits R, M, and S. Because *BpmI* is quite distinct to other type IIs restriction enzymes, it is proposed that *BpmI* belongs to a subgroup of type II restriction enzymes called type II<sub>f</sub> (f stands for fusion of restriction-modification domains).

[0016] To generate a premodified expression host, the *BpmIM1* gene was amplified in PCR and cloned in *E. coli* strain ER2566. *BpmI* M1 methylase also modifies *XhoI* site. *XhoI* recognition sequence 5' CTCGAG 3' is similar to *BpmI* recognition sequence 5' CTGGAG 3' with only one base difference. It was concluded that *BpmI* M1 methylase may recognize the sequence 5' CTNNAG 3' and possibly modify the adenine base to create N6-adenine in the symmetric sequence.

[0017] The expression of 3030-bp *BpmIRM* gene was quite difficult because of the large size of the PCR product. The *BpmIRM* gene was first amplified by *Taq* DNA polymerase and cloned into the premodified host, but no *BpmI* activity was detected. To improve the fidelity of PCR reaction, Deep Vent DNA polymerase was used in PCR. Among 18 clones with the insert, only one clone (#4) displayed partial *BpmI* activity. This clone was sequenced and confirmed to contain wild type sequence.

## BRIEF DESCRIPTION OF THE DRAWINGS

[0018]

Figure 1 Gene organization of *BpmI* restriction-modification system. Genes *BpmIRM* and *BpmIM1* code for *BpmI* endonuclease (*BpmI* endonuclease-methylase fusion protein and *BpmI* M1, respectively. *BpmI*-Δ#1, *BpmI*-Δ#2, and *BpmI*-Δ#3 are deletion mutants with deletions in the methylation or specificity domains.

Figure 2 DNA sequence of *BpmI* M1 methylase gene (*BpmIM1*) (SEQ ID NO:1) and its encoded amino acid sequence (SEQ ID NO:2).

Figure 3 DNA sequence of *BpmI* endonuclease gene (*BpmIRM*) (SEQ ID NO:3) and its encoded amino acid sequence (SEQ ID NO:4).

Figure 4 Recombinant *BpmI* endonuclease activity in column fractions following heperin Sepharose chromatography. Lane 1: purified native *BpmI* endonuclease; lanes 2 to 23: heperin Sepharose column fractions. Fractions 11 to 14 gave rise to complete *BpmI* digestion of λ DNA. The remaining fractions contain no or partial *BpmI* activity. Lane 24: 1 kb DNA size marker.

**DETAILED DESCRIPTION OF THE INVENTION**

[0019] The method described herein by which the *BpmI* methylase gene and the *BpmI* restriction endonuclease genes are preferably cloned and expressed in *E. coli* employ the following steps:

**1. Preparation of genomic DNA and restriction digestion of genomic DNA.**

[0020] Genomic DNA is prepared from *Bacillus pumilus* (New England Biolabs collection #711) by the standard procedure. Five µg genomic DNA is digested partially with 2, 1, 0.5, and 0.25 units of *ApoI* (recognition sequence R/AATY). Genomic DNA fragments in the range of 2-10 kb are purified through a low-melting agarose gel. Genomic and pBR322 DNA are also digested with *AatII*, *BamHI*, *ClaI*, *EagI*, *EcoRI*, *HindIII*, *NdeI*, *NheI*, *SalI*, and *SphI*, respectively, however, no methylase positive clones were obtained.

**2. Construction of *ApoI* partial genomic DNA library and challenge of library with *BpmI*.**

[0021] The *ApoI* partial DNA fragments are ligated to *EcoRI* digested and CIP treated pBR322 vector. The ligated DNA is transferred into *E. coli* RR1 competent cells by electroporation. Transformants are pooled and amplified. Plasmid DNA is prepared from the cells and challenged with *BpmI*. Following *BpmI* digestion, the challenged DNA is transformed into RR1 cells. Survivors are screened for resistance to *BpmI* digestion. Two resistant clones, #18 and #26, were identified to be resistant to *BpmI* digestion. *AatII*, *BamHI*, *ClaI*, *EagI*, *EcoRI*, *HindIII*, *NdeI*, *NheI*, *SalI*, and *SphI* digested genomic DNA were also ligated to pBR322 with compatible ends and genomic DNA libraries are constructed. However, no apparent *BpmI* resistant clones were discovered from these libraries.

**3. Subcloning and DNA sequencing of the resistant clone.**

[0022] One resistant clone #26 contained an insert of about 3.1 kb. The forward and reverse primers of pUC19 were used to sequence the insert. Three *ApoI* and one *HindIII* fragments were subcloned in pUC19 and sequenced. The entire insert was sequenced by primer walking. A methylase gene with high homology to amino-methyltransferase is found within the insert which is name *BpmI* M1 gene. The *BpmI*M1 gene is 1,650 bp, encoding a 549-amino acid protein with predicted molecular mass of 63,702 daltons.

**4. Cloning of *BpmI* restriction endonuclease gene (*BpmIRM*) by Inverse PCR.**

[0023] In accordance with the present invention, it was determined that there was one partial open reading frame upstream of *BpmI*M1 gene that has 31% amino acid sequence identity to another restriction enzyme *Eco57I* with similar recognition sequence (*Eco57I* recognition sequence: 5'CTGAAG N16/N14; A. Janulaitis et al. *Nucl. Acids Res.* 20: 6051-6056 (1992); *BpmI* recognition sequence: 5'CTGGAG N16/N14). Genomic DNA is digested with restriction enzymes. The digested DNA is ligated at a low DNA concentration and then used for inverse PCR amplification of *BpmIRM* gene. Inverse PCR products are derived, gel-purified from low-melting agarose and sequenced. After four rounds of inverse PCR reactions, an open reading frame of 3,030 bp was found upstream of *BpmI* M1 methylase gene, which encoded a 1,009-amino acid protein with predicted molecular mass of 116,891 daltons. This is one of the largest restriction enzyme discovered so far. By amino acid sequence comparison of *BpmI* endonuclease with all known proteins in GenBank protein database, it is discovered that *BpmI* endonuclease is a fusion of two distinct elements with a possible structural domains of restriction-methylation-specificity (R-M-S). This domain organization is analogous to the type I restriction-modification system with three distinct subunits, restriction, methylation, and specificity (R, M, and S). Because *BpmI* is quite distinct to other type IIs restriction enzymes, it is suggested that *BpmI* belongs to a subgroup of type II restriction enzymes called type II<sub>f</sub> (f stands for fusion of restriction-modification-specificity domains).

**5. Expression of *BpmI*M1 gene in *E. coli*.**

[0024] Two primers are synthesized to amplify *BpmI*M1 gene in PCR. Following digestion with *BamHI* and *SphI*, the PCR product is ligated into pACYC184 with the compatible ends. The ligated DNA is transformed into ER2566 competent cells. Plasmids with *BpmI*M1 gene inserts are tested for resistance to *BpmI* digestion. Two out of 18 clones were found to be resistant to *BpmI* digestion, indicating efficient *BpmI* M1 expression in *E. coli* cells and *BpmI* site modification on the expression plasmid. The host cell ER2566 [pACYC-*BpmI*M1] is used for expression of *BpmIRM* gene.

[0025] *BpmI* M1 methylase also modifies *XhoI* site. *XhoI* recognition sequence 5'CTCGAG3' is similar to *BpmI* recognition sequence 5'CTGGAG3' with only one base difference. It is concluded that *BpmI* M1 methylase may recognize

the sequence 5'CTNAG3' and modify the adenine base to generate N6-adenine in the symmetric sequence.

#### 6. Expression of *BpmI*RM gene in *E. coli* using a T7 expression vector.

[0026] The 3,030-bp *BpmI*RM gene was amplified in PCR using Taq DNA polymerase, digested with *Bam*HI and ligated into *Bam*HI-digested T7 expression vectors pAll17 and pET21a. After transformation of the ligated DNA into ER2566 [pACYC-*BpmI*M1], transformants were screened for the endonuclease gene insert. Seven out of 72 clones contained the insert with correct orientation. However, no *BpmI* activity was detected in cell extracts of IPTG-induced cells. This is probably due to mutations introduced during the PCR process.

[0027] To reduce the mutation frequency, Deep Vent® DNA polymerase was used in PCR reactions to amplify the 3030-bp *BpmI*RM gene. The PCR product was digested with *Bam*HI and *Xba*I and ligated to T7 expression vectors pAll17 and pET21a. Eighteen out of 36 clones contain the correct size insert. Ten ml cell culture for all 18 clones were induced with IPTG and cell extracts were prepared and assayed for *BpmI* activity. Clone #4 displayed partial *BpmI* activity.

#### 7. Partial purification of recombinant *BpmI* activity.

[0028] Five hundred ml of cell culture was made for the expression clone #4 ER2566 [pACYC-*BpmI*M1, pET21a-*BpmI*RM]. Cell extract (40 ml) containing *BpmI* was purified through a heparin Sepharose column. Proteins were eluted with a NaCl gradient of 50 mM to 1 M. Fractions 6 to 27 are assayed for *BpmI* activity on  $\lambda$  DNA. It was found that fractions 15 to 18 contained the most active *BpmI* activity (Figure 4). The yield was estimated at 1,800 units of *BpmI* per gram of wet *E. coli* cells. The specific activity was estimated at 24,000 units per mg of protein.

[0029] The present invention is further illustrated by the following Examples. These Examples are provided to aid in the understanding of the invention and are not construed as a limitation thereof.

[0030] The references cited above and below are hereby incorporated by reference herein.

### EXAMPLE 1

#### CLONING OF *BpmI* RESTRICTION-MODIFICATION SYSTEM IN *E. COLI*

##### 1. Preparation of genomic DNA and restriction digestion of genomic DNA.

[0031] Genomic DNA is prepared from *Bacillus pumilus* (New England Biolabs collection #711) by the standard procedure consisting the following steps:

(a) cell lysis by addition of lysozyme (2 mg/ml final), sucrose (1% final), and 50 mM Tris-HCl, pH 8.0;

(b) cell lysis by addition of 10% SDS (final concentration 0.1%);

(c) cell lysis by addition of 1% Triton X-100 and 62 mM EDTA, 50 mM Tris-HCl, pH 8.0;

(d) phenol-CHCl<sub>3</sub> extraction of DNA 3 times (equal volume) and CHCl<sub>3</sub> extraction one time;

(e) DNA dialysis in 4 liters of TE buffer, change 3x; and

(f) RNA was removed by RNase A treatment and the genomic DNA was precipitated in ethanol and resuspended in TE buffer;

[0032] Five  $\mu$ g genomic DNA was digested partially with 2, 1, 0.5, and 0.25 units of *Apo*I (recognition sequence RV AATTY) at 50°C for 30 min. Genomic DNA fragments in the range of 2-10 kb were purified through a 1% low-melting agarose gel. Genomic and pBR322 DNA were also digested with *Aat*II, *Bam*HI, *Cla*I, *Eag*I, *Eco*RI, *Hind*III, *Nde*I, *Nhe*I, *Sal*I, and *Sph*I, respectively. Genomic DNA fragments were ligated to pBR322 with compatible ends.

##### 2. Construction of *Apo*I partial genomic DNA library and challenge of library with *BpmI*.

[0033] The *Apo*I partial DNA fragments were ligated to *Eco*RI digested and CIP treated pBR322 vector. The ligated DNA was dialyzed by drop dialysis on 4 L of distilled water and transferred into *E. coli* RR1 competent cells by electroporation. *Ap*<sup>R</sup> transformants were pooled and amplified. Plasmid DNA was prepared from the overnight cells and

challenged with *BpmI*. Following *BpmI* digestion, the challenged DNA was transformed into RR1 cells. Ap<sup>R</sup> survivors were screened for resistance to *BpmI* digestion. A total of 36 plasmid mini-preparations were made. Two resistant clones, #18 and #26, were identified to be resistant to *BpmI* digestion. *AatII*, *BamHI*, *ClaI*, *EagI*, *EcoRI*, *HindIII*, *NdeI*, *NheI*, *SacI*, and *SphI* digested genomic DNA were also ligated to pBR322 with compatible ends and genomic DNA libraries were constructed. However, no apparent *BpmI* resistant clones were discovered from these libraries after screening more than 144 clones.

### 3. Subcloning and DNA sequencing of the resistant clone.

[0034] One resistant clone #26 contains an insert of about 3.1 kb. The forward and reverse primers of pUC19 were used to sequence the insert. Three *ApoI* and one *HindIII* fragments were gel-purified and subcloned in pUC19 and sequenced. The rest of the insert was sequenced by primer walking. A methylase gene with high homology to amino-methyltransferase (N6-adenine methylase) was found within the insert which was named *BpmI* M1 gene. The *BpmI* M1 gene is 1,650 bp, encoding a 549-amino acid protein with predicted molecular mass of 63,702 daltons.

### 4. Cloning of *BpmI* restriction endonuclease gene (*BpmIRM*) by inverse PCR.

[0035] There is one partial open reading frame upstream of *BpmI* M1 gene that has 31% amino acid sequence identity to another restriction enzyme *Eco57I* with similar recognition sequence (*Eco57I* recognition sequence: 5'CTGAAG N16/N14; A. Janulaitis et al. *Nucl. Acids Res.* 20:6051-6056 (1992); *BpmI* recognition sequence: 5'CTGGAG N16/N14). Genomic DNA was digested with restriction enzymes *Asel*, *BclI*, *HaeIII*, *HpaII*, *MboI*, *MseI*, *NlaIII*, *PaeI*, and *Tsp509I*. The digested DNA was ligated at a low DNA concentration at 2 µg/ml and then used for inverse PCR amplification of *BpmIR* gene. The sequence of the inverse PCR primers was the following:

5' gtggaaacggaccgtattatgggtt 3' (232-34) (SEQ ID NO:5)

5' caccagtaaataacaggttattcc 3' (232-35) (SEQ ID NO:6)

[0036] Inverse PCR conditions were 94°C 1 min, 55°C 1 min, 72°C 2 min for 35 cycles. Inverse PCR products were derived from *HaeIII* and *NlaIII* templates, gel-purified from low-melting agarose and sequenced using primers 232-34 and 35.

[0037] The primers for second round of inverse PCR were the following:

5' ttcgtagcaagtacggtccatatcagt 3' (233-76) (SEQ ID NO:7)

5' ccgtatgtacttgataggaataacctg 3' (233-77) (SEQ ID NO:8)

[0038] Genomic DNA was digested with *Asel*, *BclI*, *BsrFI*, *BstNI*, *EcoRI*, *HincII*, *HindIII*, *HpaII*, *NcoI*, *PaeI*, *PvuI*, *TaqI*, *TthI*, and *XbaI*. The digested DNA was ligated at a low DNA concentration at 2 µg/ml and then used for inverse PCR amplification of *BpmIR* gene. Inverse PCR conditions were 94°C 1 min, 55°C 1 min, 72°C 2 min for 35 cycles. Inverse PCR products were derived from *Asel*, *HindIII*, *HpaII*, and *TaqI* templates, gel-purified from low-melting agarose and sequenced using primers 233-76 and 77.

[0039] The primers for third round of inverse PCR were the following:

5' aggaactaagaaagttcatagctg 3' (234-61) (SEQ ID NO:9)

5' atgcggtattatataaccaacag 3' (234-62) (SEQ ID NO:10)

5 [0040] Genomic DNA was digested with *Afl*III, *Bsp*HI, *Bst*NI, *Eco*RI, *Hae*II, *Hin*P1I, *Hha*II, *Hind*III, *Sst*I, and *Xmn*I. The digested DNA was ligated at a low DNA concentration at 2 µg/ml and then used for inverse PCR amplification of *Bpm*I/R gene. Inverse PCR conditions were 94°C 1 min, 55°C 1 min, 72°C 2 min for 35 cycles. Inverse PCR products were derived from *Hin*P1I and *Xmn*I templates, gel-purified from low-melting agarose and sequenced using primers 234-61 and 62.

10 [0041] The primers for the fourth round of inverse PCR were the following:

5' tgacgtcctcttcacctaattcgg 3' (235-50) (SEQ ID NO:11)

15

5' gagtttggaagatagaaccattg 3' (235-51) (SEQ ID NO:12)

[0042] Genomic DNA was digested with *Apo*I, *Bst*BI, *Bst*YI, *Cla*I, *Eco*RI, *Nde*I, *Rsa*I, *Sau*3AI, *Ssp*I, *Taq*I, and *Xmn*I. The digested DNA was ligated at a low DNA concentration at 2 µg/ml and then used for inverse PCR amplification of *Bpm*I/R gene. Inverse PCR conditions were 94°C 1 min, 55°C 1 min, 72°C 2 min for 35 cycles. Inverse PCR products were derived from *Apo*I, *Cla*I, *Nde*I, *Rsa*I, *Ssp*I, and *Taq*I templates, gel-purified from low-melting agarose and sequenced using primers 235-50 and 51. The *Cla*I fragment (2.4 kb) further extends upstream of *Bpm*I/RM gene. The rest of the *Cla*I fragment was sequenced using primer walking.

25 [0043] After four rounds of inverse PCR reactions, an open reading frame of 3,030 bp was found upstream of *Bpm*I M1 methylase gene, which encodes a 1,009-amino acid protein with predicted molecular mass of 116,891 daltons. This is one of the largest restriction enzyme discovered so far. By amino acid sequence comparison of *Bpm*I endonuclease with all known proteins in GenBank protein database, it was discovered that *Bpm*I endonuclease is a fusion of two distinct elements with a possible structural domains of restriction-methylation-specificity (R-M-S). This domain organization is analogous to the type I restriction-modification system with three distinct subunits, restriction, methylation, and specificity (R, M, and S). Because *Bpm*I is quite distinct to other type IIs restriction enzymes, it is proposed that *Bpm*I belongs to a subgroup of type II restriction enzymes called type II<sub>f</sub> (f stands for fusion of restriction-modification-specificity domains)

35 5. Expression of *Bpm*I/M1 gene in *E. coli*.

[0044] Two primers are synthesized to amplify *Bpm*I/M1 gene in PCR. The primer sequences are:

40

forward:

5' agcggatccggaggtaaataaatgaatcaattaattgaaaatgttaat 3'

(238-177) (SEQ ID NO:13)

45

reverse:

50

5' aaggggggcatgcttatacttatttcttcgttctattgtttct 3' (238-178)

(SEQ ID NO:14)

55

[0045] Following digestion with *Bam*HI and *Sph*I, the PCR product was ligated into pACYC184 with the compatible ends. The ligated DNA was transformed into ER2566 competent cells. Cm<sup>R</sup> transformants were plated at 37°C overnight. Plasmids with *Bpm*I/M1 gene inserts were tested for resistance to *Bpm*I digestion. Two out of 18 clones showed

full resistance to *BpmI* digestion, indicating efficient *BpmI* M1 expression in *E. coli* cells and *BpmI* site modification on the expression plasmid. The host cell ER2566 [pACYC-*BpmI*M1] was used for expression of *BpmI*RM gene.

[0046] *BpmI* M1 methylase also modifies *XhoI* site. *XhoI* recognition sequence 5'CTCGAG3' is similar to *BpmI* recognition sequence 5'CTGGAG3' with only one base difference. It is concluded that *BpmI* M1 methylase may recognize the sequence 5'CTNNAG3' and modify the adenine base to generate N6-adenine in the symmetric recognition sequence.

#### 6. Expression of *BpmI*RM gene in *E. coli* using a T7 expression vector.

[0047] Two primers were synthesized to amplify the *BpmI*RM gene. The primer sequences were:

5' caaggatccggaggtaaataaatgcatataagtgagttagtagataaatac 3'  
(247-217) (SEQ ID NO:15)

5' ttaggatcctcatttttcttctcctaacgccgctgt 3' (238-182)  
(SEQ ID NO:16)

[0048] The 3,030-bp *BpmI*RM gene was amplified in PCR using Taq DNA polymerase, digested with *Bam*HI and ligated into *Bam*HI-digested T7 expression vectors pAll17 and pET21a. After transformation of the ligated DNA into ER2566 [pACYC-*BpmI*M1], Ap<sup>R</sup> Cm<sup>R</sup> transformants were screened for the endonuclease gene insert. Seven out of 72 clones contained the insert with correct orientation. However, no *BpmI* activity was detected in cell extracts of IPTG-induced cells. This was probably due to mutations introduced during the PCR process.

[0049] To reduce the mutation frequency, Deep Vent® DNA polymerase was used in PCR reactions to amplify the 3,030-bp *BpmI*RM gene. The forward primer incorporated an *XbaI* site and its sequence is the following:

5' caccaatctagaggaggtaaataaatgcatataagtgagttagtagataaatac 3' (238-181) (SEQ ID NO:17)

[0050] PCR was performed using primers 238-181, 238-182, and Deep Vent® DNA polymerase. The PCR conditions were 94°C 5 min for one cycle; 94°C 1 min, 55°C 1.5 min, 72°C 8 min for 20 cycles. The PCR product was purified through a Qiagen spin column and digested with *Bam*HI and *XbaI* and ligated to T7 expression vectors pAll17 and pET21a with compatible ends. Eighteen out of 36 clones contain the correct size insert. Ten ml cell culture for all 18 clones containing inserts were induced with IPTG for 3h and cell extracts were prepared by sonication and assayed for *BpmI* activity. Clone #4 displayed partial *BpmI* activity. Because this gene was derived by PCR cloning, the entire *BpmI*RM fusion gene was sequenced on both strands and it was confirmed to be wild type sequence.

#### 7. Partial purification of recombinant *BpmI* activity.

[0051] Five hundred ml of cell culture was made for the expression clone #4 ER2566 [pACYC-*BpmI*M1, pET21a-*BpmI*RM]. The late log cells were induced with IPTG and Cell extract (40 ml) containing *BpmI* was purified through a heparin Sepharose column. Proteins were eluted with a NaCl gradient of 50 mM to 1 M. Fractions 6 to 27 contained the most protein concentration and were assayed for *BpmI* activity on λ DNA. It was found that fractions 15 to 18 contained the most active *BpmI* activity (Figure 4). The yield was estimated at 1,800 units of *BpmI* per gram of wet *E. coli* cells. The specific activity was estimated at 24,000 units per mg of protein. Proteins from fractions 15 to 18 were analyzed on a SDS-PAGE gel and protein bands were stained with Gelcode blue stain. A protein band corresponding

to ~115 kDa was detected on the protein gel, in close agreement with the predicted size of 117 kDa.

[0052] The *E. coli* strain ER2566 [pACYC-BpmIM1, pET21at-BpmIRM] has been deposited under the terms and conditions of the Budapest Treaty with the American Type Culture Collection on October 12, 2000 and received Accession No. PTA-2598.

## Example 2

### Deletion of the methylase portion of *BpmI* RM fusion protein

[0053] Two primers were synthesized to amplify the putative endonuclease domain with deletion of the methylase and specificity domains. The deletion clone thus contains only the R portion and the M and S portions were removed. The forward primer was 238-181 as described above. The reverse primer had the following sequence with a *XhoI* site at the 5' end:

5' tgaaatctcgagttatcctgatccacaacatatatctgctat 3' (244-95)  
(SEQ ID NO:18)

[0054] The deletion junction was in motif I of  $\gamma$  type N6 adenine methylase. The  $\gamma$  type N6 adenine methylases contain conserved motifs of X, I, II, III, IV, V, VI, VII, VIII. The specificity domain (TRD) is located after motif VIII. The *BpmI* deletion clone (*BpmI*- $\Delta$ #1) still carried motifs X and part of motif I. The specificity domain after motif VIII was also deleted (the remaining portion is shown in Figure 1).

[0055] PCR was performed using primers 238-181 and 244-95 and Taq plus Vent® DNA polymerase (94°C 1 min, 60°C 1 min, and 72°C 1 min for 25 cycles). The PCR product was digested with *XbaI* and *XhoI* and cloned into a T7 expression vector pET21b. Sixteen clones out of 36 screened contained the correct size insert and the cells were induced with IPTG for 3h. Cell extract was prepared by sonication and assayed for *BpmI* activity on  $\lambda$  DNA. However, no apparent *BpmI* digestion pattern was detected. Only non-specific nuclease was detected in cell extract, resulting in a smearing of DNA substrate. It was concluded that deletion of the methylase and specificity portion of the *BpmIRM* fusion protein abolished *BpmI* restriction activity.

[0056] To further confirm the above result, another deletion clone was constructed that deleted methylase motifs IV, V, VI, VII, VIII, and the specificity domain. This *EcoRI* fragment deletion mutant contains 1,521 bp (507 amino acid) deletion at the C-terminus half of the fusion protein (*BpmI*- $\Delta$ #2). IPTG-induced cell extract of this mutant also did not display *BpmI* endonuclease activity.

[0057] To delete the specificity domain (target-recognizing domain, TRD), a *HindIII* fragment of 579 bp (193 amino acid) was deleted from the C-terminus of *BpmI* RM fusion endonuclease (*BpmI*- $\Delta$ #3). IPTG-induced cell extract of the TRD deletion mutant did not show any *BpmI* endonuclease activity. However, the mutant protein displayed non-specific nuclease activity. It was concluded that the specificity (TRD) domain is also required for *BpmI* endonuclease activity. Deletion of the specificity (TRD) domain may abolish or reduce its DNA binding affinity and specificity. By swapping in of other N6 methylase and specificity domains, one may be able to create new enzyme specificity.

## Example 3

### Generation of new enzyme specificity using *BpmI* RM fusion protein

[0058] Since *BpmI* endonuclease consists of three domains (R-M-S), it is possible to plug in other methylation-specificity domains to create a new enzyme specificity. The *BpmIRM* fusion gene is cloned in a T7 expression vector as described in Example 1. Plasmid DNA is prepared. The  $\gamma$  type N6 adenine methylases contain conserved motifs of X, I, II, III, IV, V, VI, VII, VIII (Malone T. et al. *J.Mol.Biol* 253:618-632 (1995)). Motifs X through VIII and TRD are deleted and a DNA linker coding for one or more bridging amino acids is inserted with a restriction site, preferably blunt (for example *SmaI* site). The number of amino acids will differ from one system to the next and can be determined by routine experimentation. The goal is to provide sufficient steric space for the introduction of the new M-S domains. DNA coding for other  $\gamma$  type N6 adenine methylases containing motifs of X, I, II, III, IV, V, VI, VII, VIII and TRD are ligated to the digested blunt site (in frame) of the *BpmI* deletion clone. The ligated DNA is transformed into a non-T7 expression vector. After the insert is verified, the plasmid containing new methylation-specificity domains is transformed into a T7 expression host and induced with IPTG. Cell extract is assayed on plasmid and phage DNA and analyzed

for new restriction activity.

## SEQUENCE LISTING

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<120> Method for Cloning and Expression of BpmI Restriction Endonuclease in E .coli

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5	gat tta gta tat gaa act gaa gaa ggg cta att ttg aca ctt aaa gca Asp Leu Val Tyr Glu Thr Glu Glu Gly Leu Ile Leu Thr Leu Lys Ala 420 425 430			1296
10	aaa aga aat atc ttg gag aat aat ttg ttt ggt gtt gat gtt aat cca Lys Arg Asn Ile Leu Glu Asn Asn Leu Phe Gly Val Asp Val Asn Pro 435 440 445			1344
15	tac gct gtt gaa gta gct gag ttc agt tta tta tta aag cta tta gaa Tyr Ala Val Glu Val Ala Glu Phe Ser Leu Leu Lys Leu Leu Glu 450 455 460			1392
20	ggg gag aat gag gca tcg gtt aat aat ttc att cac gag cat gag gat Gly Glu Asn Glu Ala Ser Val Asn Asn Phe Ile His Glu His Glu Asp 465 470 475 480			1440
25	aaa ata tta ccg gat tta aca tct att att aaa tgt gga aac agc tta Lys Ile Leu Pro Asp Leu Thr Ser Ile Ile Lys Cys Gly Asn Ser Leu 485 490 495			1488
30	gta gat aat aag ttt ttt gaa ttc atg cca gaa tcg tta gag gac gat Val Asp Asn Lys Phe Phe Glu Phe Met Pro Glu Ser Leu Glu Asp Asp 500 505 510			1536
35	gaa atc tta ttt aag gct aat cca ttt gaa tgg gaa gag gag ttt cca Glu Ile Leu Phe Lys Ala Asn Pro Phe Glu Trp Glu Glu Glu Phe Pro 515 520 525			1584
40	gat att atg gca aat ggt ggc ttt gat gct att ata gga aat cca cct Asp Ile Met Ala Asn Gly Gly Phe Asp Ala Ile Ile Gly Asn Pro Pro 530 535 540			1632
45	tat gtt cga ata cag aac atg aaa aaa tat agt cct gag gaa att gaa Tyr Val Arg Ile Gln Asn Met Lys Lys Tyr Ser Pro Glu Glu Ile Glu 545 550 555 560			1680
50	tat tat caa tca aaa gac tct gaa tat act gtt gca aaa aaa gaa aca Tyr Tyr Gln Ser Lys Asp Ser Glu Tyr Thr Val Ala Lys Lys Glu Thr 565 570 575			1728
55	gtt gac aag tat ttt tta ttt att gag aga gca tta ata tta ctc aat Val Asp Lys Tyr Phe Leu Phe Ile Glu Arg Ala Leu Ile Leu Leu Asn 580 585 590			1776
60	cct act ggg ctg ttg ggt tat ata ata ccg cat aaa ttc ttt att aca Pro Thr Gly Leu Leu Gly Tyr Ile Ile Pro His Lys Phe Phe Ile Thr 595 600 605			1824
65	aaa ggt ggt aag gaa cta aga aag ttc ata gct gaa aaa cat caa ata Lys Gly Gly Lys Glu Leu Arg Lys Phe Ile Ala Glu Lys His Gln Ile 610 615 620			1872
70	tca aaa att ata aat ttt ggt gtt aca cag gtc ttt cca gga aga gcg Ser Lys Ile Ile Asn Phe Gly Val Thr Gln Val Phe Pro Gly Arg Ala 625 630 635 640			1920
75	aca tat acg gct att tta att atc caa gca aat aaa atg gca cag ttc Thr Tyr Thr Ala Ile Leu Ile Ile Gln Ala Asn Lys Met Ala Gln Phe 645 650 655			1968

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5	aag tat aag aaa gta agt aat ata tca gca gaa acc cta gat tct gaa Lys Tyr Lys Lys Val Ser Asn Ile Ser Ala Glu Thr Leu Asp Ser Glu 660 665 670	2016
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10	ata ttt tta tct cct gaa aca gaa gct gtt ttt act aaa ttt aca gaa Ile Phe Leu Ser Pro Glu Thr Glu Ala Val Phe Thr Lys Phe Thr Glu 690 695 700	2112
15	gct caa ttt gag aaa ctt gga gaa atc act gat ata agt gta gga cta Ala Gln Phe Glu Lys Leu Gly Glu Ile Thr Asp Ile Ser Val Gly Leu 705 710 715 720	2160
	caa aca agc gct gat aaa ata tat att ttt att cct gaa aat gaa act Gln Thr Ser Ala Asp Lys Ile Tyr Ile Phe Ile Pro Glu Asn Glu Thr 725 730 735	2208
20	tca gat aca tat ata ttt aat tat aaa ggg aaa aga tat gaa ata gaa Ser Asp Thr Tyr Ile Phe Asn Tyr Lys Gly Lys Arg Tyr Glu Ile Glu 740 745 750	2256
25	aaa tct ata tgt tgc cca gct atc tat gac tta tct ttt ggt tct ttt Lys Ser Ile Cys Cys Pro Ala Ile Tyr Asp Leu Ser Phe Gly Ser Phe 755 760 765	2304
	gaa agc att cag gga aat gca caa atg ata ttc cct tat gaa atc aga Glu Ser Ile Gln Gly Asn Ala Gln Met Ile Phe Pro Tyr Glu Ile Arg 770 775 780	2352
30	gat gaa gaa gca tat cta cta gag gaa gaa acg ctt gaa aat gat tat Asp Glu Glu Ala Tyr Leu Leu Glu Glu Glu Thr Leu Glu Asn Asp Tyr 785 790 795 800	2400
35	cct ctt gct tgg aat tat ttg aat gag ttt aaa gaa gct ctt gaa aaa Pro Leu Ala Trp Asn Tyr Leu Asn Glu Phe Lys Glu Ala Leu Glu Lys 805 810 815	2448
	aga agc tta caa ggc cgt aat ccg aaa tgg tat caa tat ggt cgg tcc Arg Ser Leu Gln Gly Arg Asn Pro Lys Trp Tyr Gln Tyr Gly Arg Ser 820 825 830	2496
40	caa agt tta tca aaa ttt cat gat aaa gaa aaa ctg ata tgg acc gta Gln Ser Leu Ser Lys Phe His Asp Lys Glu Lys Leu Ile Trp Thr Val 835 840 845	2544
45	ctt gct acg aaa ccc ccg tat gta ctt gat agg aat aac ctg tta ttt Leu Ala Thr Lys Pro Pro Tyr Val Leu Asp Arg Asn Asn Leu Leu Phe 850 855 860	2592
50	act ggt ggt gga aac gga ccg tat tat ggt tta att aac caa tct att Thr Gly Gly Gly Asn Gly Pro Tyr Tyr Gly Leu Ile Asn Gln Ser Ile 865 870 875 880	2640
	tac tct ttg cat tat ttt tta ggt att ctt tca cat cct gta ata gaa Tyr Ser Leu His Tyr Phe Leu Gly Ile Leu Ser His Pro Val Ile Glu 885 890 895	2688

55

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agt atg gta aaa gca agg gcc agt gaa ttt agg gga tca tat tat tct 2736  
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 900 905 910  
 5  
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 gat gat caa gat gag gta gac aaa tat aat acg gtg gtc aca aca gta 2832  
 Asp Asp Gln Asp Glu Val Asp Lys Tyr Asn Thr Val Val Thr Thr Val  
 930 935 940  
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 Glu Lys Leu Ile Ile Thr Thr Asp Arg Ile Lys Ser Glu Ser Asn Gly  
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 20  
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 25  
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 Leu Ile Gln Val Ile Asn Glu Leu Tyr Asn Ile Ser Asp Glu Glu Tyr  
 980 985 990  
 3024  
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 20 25 30  
 45  
 Asp Pro Leu Leu Lys Ser Leu Gly Trp Asp Val Asp Asn Thr Lys Gly  
 35 40 45  
 50  
 Lys Thr His Ile Leu Arg Asp Val Ile Gln Glu Glu Tyr Ile Glu Ile  
 50 55 60  
 55  
 Lys Asp Glu Glu Thr Lys Lys Asn Pro Asp Tyr Thr Leu Arg Ile Asn  
 65 70 75 80  
 Gly Thr Arg Lys Leu Phe Val Glu Val Lys Lys Pro Ser Phe Asn Ile

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15	Tyr Asp Cys Arg Tyr Thr Pro Asp Lys Ser Asp Asn Glu His Ile Ala 130 135 140		
20	Arg Tyr Lys Val Phe Ser Tyr Glu Glu Tyr Glu Glu Ala Phe Asp Glu 145 150 155 160		
25	Ile Lys Asp Ile Ile Ser Tyr Glu Ser Ala Asn Ser Gly Ala Leu Asp 165 170 175		
30	Glu Met Phe Asp Val Asn Thr Arg Val Gly Glu Thr Phe Asp Glu Tyr 180 185 190		
35	Phe Leu Gln Gln Ile Glu Asn Trp Arg Glu Lys Leu Ala Lys Thr Ala 195 200 205		
40	Ile Lys Asn Asn Thr Glu Leu Gly Glu Glu Asp Val Asn Phe Ile Val 210 215 220		
45	Gln Arg Leu Leu Asn Arg Ile Ile Phe Leu Arg Val Cys Glu Asp Arg 225 230 235 240		
50	Thr Ile Glu Lys Tyr Glu Thr Ile Lys Ser Ile Lys Asn Tyr Glu Glu 245 250 255		
55	Leu Lys Asp Leu Phe Gln Lys Ser Asp Arg Lys Phe Asn Ser Gly Leu 260 265 270		
	Phe Asp Phe Ile Asp Asp Thr Leu Leu Leu Glu Val Glu Ile Asp Ser 275 280 285		
	Asn Val Leu Ile Glu Ile Phe Ser Asp Leu Tyr Phe Pro Gln Ser Pro 290 295 300		
	Tyr Asp Phe Ser Val Val Asp Pro Thr Ile Leu Ser Gln Ile Tyr Glu 305 310 315 320		
	Arg Phe Leu Gly Gln Glu Ile Ile Ile Glu Ser Gly Gly Thr Phe His 325 330 335		

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5 Ile Thr Glu Ser Pro Glu Val Ala Ala Ser Asn Gly Val Val Pro Thr  
340 345 350

Pro Lys Ile Ile Val Glu Gln Ile Val Lys Asp Thr Leu Thr Pro Leu  
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10 Thr Glu Gly Lys Lys Phe Asn Glu Leu Cys Asn Leu Lys Ile Ala Asp  
370 375 380

15 Ile Cys Cys Gly Ser Gly Thr Phe Leu Ile Ser Ser Tyr Asp Phe Leu  
385 390 395 400

Val Glu Lys Val Met Glu Lys Ile Ile Glu Glu Asn Ile Asp Asp Ser  
405 410 415

20 Asp Leu Val Tyr Glu Thr Glu Glu Gly Leu Ile Leu Thr Leu Lys Ala  
420 425 430

25 Lys Arg Asn Ile Leu Glu Asn Asn Leu Phe Gly Val Asp Val Asn Pro  
435 440 445

Tyr Ala Val Glu Val Ala Glu Phe Ser Leu Leu Leu Lys Leu Leu Glu  
450 455 460

30 Gly Glu Asn Glu Ala Ser Val Asn Asn Phe Ile His Glu His Glu Asp  
465 470 475 480

35 Lys Ile Leu Pro Asp Leu Thr Ser Ile Ile Lys Cys Gly Asn Ser Leu  
485 490 495

Val Asp Asn Lys Phe Phe Glu Phe Met Pro Glu Ser Leu Glu Asp Asp  
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40 Glu Ile Leu Phe Lys Ala Asn Pro Phe Glu Trp Glu Glu Glu Phe Pro  
515 520 525

45 Asp Ile Met Ala Asn Gly Gly Phe Asp Ala Ile Ile Gly Asn Pro Pro  
530 535 540

50 Tyr Val Arg Ile Gln Asn Met Lys Lys Tyr Ser Pro Glu Glu Ile Glu  
545 550 555 560

Tyr Tyr Gln Ser Lys Asp Ser Glu Tyr Thr Val Ala Lys Lys Glu Thr  
565 570 575

55

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5 Val Asp Lys Tyr Phe Leu Phe Ile Glu Arg Ala Leu Ile Leu Leu Asn  
580 585 590

Pro Thr Gly Leu Leu Gly Tyr Ile Ile Pro His Lys Phe Phe Ile Thr  
595 600 605

10 Lys Gly Gly Lys Glu Leu Arg Lys Phe Ile Ala Glu Lys His Gln Ile  
610 615 620

15 Ser Lys Ile Ile Asn Phe Gly Val Thr Gln Val Phe Pro Gly Arg Ala  
625 630 635 640

Thr Tyr Thr Ala Ile Leu Ile Ile Gln Ala Asn Lys Met Ala Gln Phe  
645 650 655

20 Lys Tyr Lys Lys Val Ser Asn Ile Ser Ala Glu Thr Leu Asp Ser Glu  
660 665 670

25 Glu Asn Thr Cys Val Tyr Ser Ser Glu Lys Tyr Asn Ser Asp Pro Trp  
675 680 685

Ile Phe Leu Ser Pro Glu Thr Glu Ala Val Phe Thr Lys Phe Thr Glu  
690 695 700

30 Ala Gln Phe Glu Lys Leu Gly Glu Ile Thr Asp Ile Ser Val Gly Leu  
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35 Gln Thr Ser Ala Asp Lys Ile Tyr Ile Phe Ile Pro Glu Asn Glu Thr  
725 730 735

Ser Asp Thr Tyr Ile Phe Asn Tyr Lys Gly Lys Arg Tyr Glu Ile Glu  
740 745 750

40 Lys Ser Ile Cys Cys Pro Ala Ile Tyr Asp Leu Ser Phe Gly Ser Phe  
755 760 765

45 Glu Ser Ile Gln Gly Asn Ala Gln Met Ile Phe Pro Tyr Glu Ile Arg  
770 775 780

50 Asp Glu Glu Ala Tyr Leu Leu Glu Glu Glu Thr Leu Glu Asn Asp Tyr  
785 790 795 800

55 Pro Leu Ala Trp Asn Tyr Leu Asn Glu Phe Lys Glu Ala Leu Glu Lys  
805 810 815

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Arg Ser Leu Gln Gly Arg Asn Pro Lys Trp Tyr Gln Tyr Gly Arg Ser  
820 825 830

5

Gln Ser Leu Ser Lys Phe His Asp Lys Glu Lys Leu Ile Trp Thr Val  
835 840 845

10

Leu Ala Thr Lys Pro Pro Tyr Val Leu Asp Arg Asn Asn Leu Leu Phe  
850 855 860

Thr Gly Gly Gly Asn Gly Pro Tyr Tyr Gly Leu Ile Asn Gln Ser Ile  
865 870 875 880

15

Tyr Ser Leu His Tyr Phe Leu Gly Ile Leu Ser His Pro Val Ile Glu  
885 890 895

20

Ser Met Val Lys Ala Arg Ala Ser Glu Phe Arg Gly Ser Tyr Tyr Ser  
900 905 910

His Gly Lys Gln Phe Ile Glu Lys Ile Pro Ile Arg Lys Ile Asp Phe  
915 920 925

25

Asp Asp Gln Asp Glu Val Asp Lys Tyr Asn Thr Val Val Thr Thr Val  
930 935 940

30

Glu Lys Leu Ile Ile Thr Thr Asp Arg Ile Lys Ser Glu Ser Asn Gly  
945 950 955 960

Pro Arg Arg Arg Met Leu Arg Arg Arg Leu Asp Ala Leu Ser Asn Gln  
965 970 975

35

Leu Ile Gln Val Ile Asn Glu Leu Tyr Asn Ile Ser Asp Glu Glu Tyr  
980 985 990

40

Thr Thr Val Leu Asn Asp Glu Met Leu Thr Ala Ala Leu Gly Glu Glu  
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       <400> 14  
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       <211> 36  
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       <400> 16  
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       <211> 54  
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       <400> 17  
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 50  
  
  
  
 55

Claims

1. Isolated DNA segment coding for the *BpmI* restriction endonuclease, wherein the isolated DNA is obtainable from *Bacillus pumilus* (New England Biolabs collection #711).
2. A recombinant DNA vector comprising a vector into which a DNA segment encoding the *BpmI* restriction endonuclease has been inserted.
3. Isolated DNA segment coding for the *BpmI* restriction endonuclease and *BpmI* methylase M1, wherein the isolated DNA is obtainable from ATCC No. PTA-2598.
4. A cloning vector which comprises the isolated DNA of claim 3.
5. A host cell transformed by the vector of claims 2 or 4.
6. A method of producing recombinant *BpmI* restriction endonuclease comprising culturing a host cell transformed with the vector of claims 2 or 4 under conditions for expression of said endonuclease.
7. A method for modifying the specificity of a target restriction-modification system comprising the steps:
  - (a) isolating DNA coding for a Type II restriction-modification system and deleting the methylation-specificity domains of said Type II restriction-modification system;
  - (b) inserting a DNA linker coding for an appropriate restriction site and one or more amino acids at the deletion site of step (a); and
  - (c) inserting an methylation-specificity fusion from a second Type II restriction-modification system adjacent the DNA linker of step (b) to form a modified target restriction-modification system.

FIG. 1

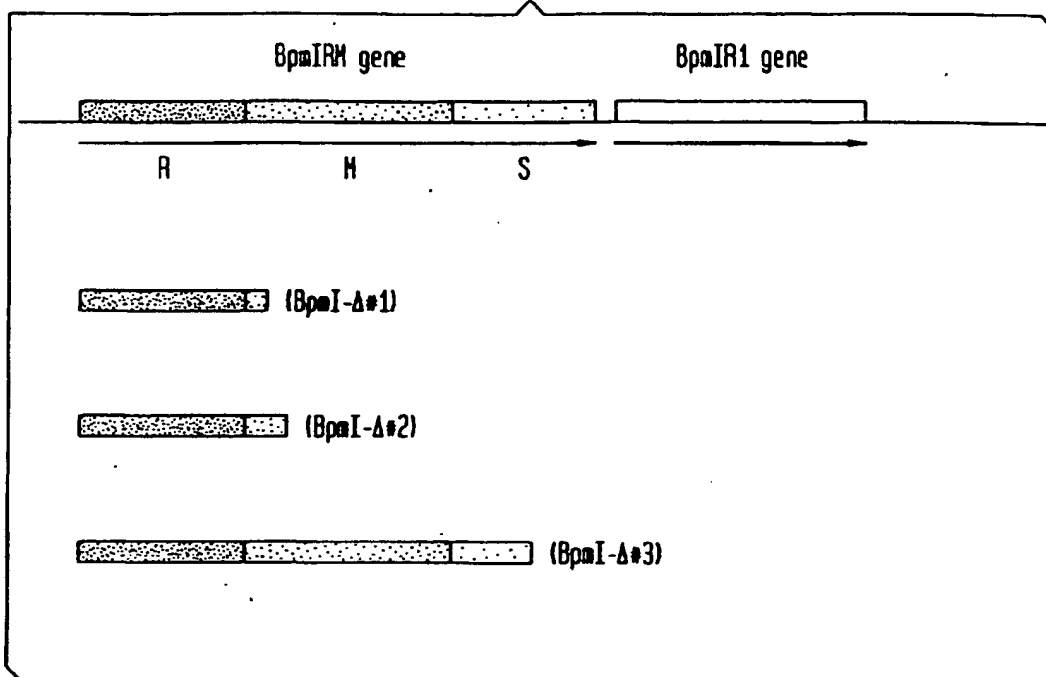


FIG. 2A

1 ATGAATCAATTAATTGAAATGTTAATCTACAAAATTAAGGGGTGGGTATTACACCCCT 60  
 H N Q L I E N V N L Q K L R G G Y Y T P  
 AAAGTTATTGCTGACTTTTATGTCAATGGAGTATTCAAGATGACACAAAGAGTGTACTT  
 61 K V I A D F L C Q W S I Q D D T K S V L 120  
 GAACCCAGTTGTGGAGATGGTAATTTTATTGAATCGGCAACTTAGGTTCAAAGAACTT  
 121 E P S C G D G N F I E S A I L R F K E L 180  
 AGTATAGATAATGAACAACCTTAAAGGAAGAATTACAGGAGTAGAGCTAATTGAAGAAGAA  
 181 S I D N E Q L K G R I T G V E L I E E E 240  
 GCTTGAAAGTTCAAAATCGAGCAAATGAGTTGGGGTTGATAAACTCAATAGTAAAT  
 241 A L K V Q N R A N E L G V D K N S I V N 300  
 AGTGACTTCTTTCAATTTGTAAGAGATAATAAGAATAAAAAATTTGATACTATTATTGGT  
 301 S D F F Q F V K D N K N K K F D T I I G 360  
 AATCCACCATTCAATAGATACCAAACTTCTGAAGAGCATCGTAGTATAGCCATGGAA  
 361 N P P F I R Y Q N F P E E H R S I A M E 420  
 ATGATGGAGGAAGTAGGTTTAAACCTAATAAATTACAAATATCTGGGTTCCATTCTA  
 421 H M E E L G L K P N K L T N I W V P F L 480  
 GTGGTATCTGCTACATTACTTAATGAACAAGGAAGATGGCTATGGTTATACCGGCTGAA  
 481 V V S A T L L N E Q G K M A M V I P A E 540  
 TTATTTCAAGTAAAGTATGCAGCAGAAACAAGATTTTTTATCAAAGTTTTTCGATCGT  
 541 L F O V K Y A A E T R I F L S K F F D R 600  
 ATCACTATAATTACATTGAAAACTTGTTTTGAAAATATCCAACAGGAAGTTATACTA  
 601 I T I I T F E K L V F E N I Q Q E V I L 660  
 CTTCTTTGTGAAAAGAAAGTTAATAAGGTAAGGAATTCGGGTTATTGAATGCAGAAC  
 661 L L C E K K V N K G K G I R V I E C E N 720  
 TTAGATGGATTAAATTCATTGATTTGTAGCTATAAATGGTTCAAATGTTAAACCTATT  
 721 L D G L N S I D F V A I N G S N V K P I 780  
 GAACACCGTACTGAAAAGTGACAAAGTATTTCTTAAACGAAGATGAAATACTTCTTTA  
 781 E H R T E K W T K Y F L N E D E I L L L 840  
 CAGAGTTTAAAGGAAGACAAACGCGTTAAAAATTGTAATGACTATTTTAAGACAGAAGT  
 841 O S L K E D K R V K N C N D Y F K T E V 900  
 GGCTTAGTTACTGGACGAAACGAATTCCTTATGATGAAAGAAAACCAAGTAAAGAATGG  
 901 G L V T G R N E F F M M K E N Q V K E W 960  
 AATCTAGAAGAATATACAATACCTGTTACAGGTAGGTCCAATCAGTTAAAGGTATAACA  
 961 N L E E Y T I P V T G R S N Q L K G I T 1020

29

FIG. 3A

ATGCATATAAGTGAGTTAGTAGATAAATACAAAGCGCATAGAAGTACTTTTTTAAACCA  
 1 M H I S E L V D K Y K A H R S T F L K P 60  
 ACTTATAATGAACTCAACTAAGGAATGATTTTATAGACCCACTTCTAAAACTTTAGGA  
 61 T Y N E T O L R N D F I D P L L K S L G 120  
 TGGGATGTTGATAATACCAAAGGAAAAACATATTCTAAGAGATGTCATTCAAGAAGAA  
 121 W D V D N T K G K T H I L R D V I O E E 180  
 TACATAGAAATAAAAGATGAGGAGACAAAGAAAAATCCAGATTATACACTTCGTATAAAC  
 181 Y I E I K D E E T K K N P D Y T L R I N 240  
 GGTACGAGAAAGCTGTTTGTAGAGGTTAAGAAACCGTCTTTTAATATTTGAAATCAGCT  
 241 G T R K L F V E V K K P S F N I L K S A 300  
 AAAGCAGCCTTCCAAACAAGAAGATATGGTTGGAGTGCTAACCTTGGTATTTTCACTACTT  
 301 K A A F O T R R Y G W S A N L G I S V L 360  
 ACAAATTTGAGCATCTAGTTATTTATGATTGTAGATATACGCTGACAAATCCGACAAT  
 361 T N F E H L V I Y D C R Y T P D K S D N 420  
 GAACATATTGCTAGATATAAAGTTTTCTTACGAGGAATATGAAGAAGCATTGATGAA  
 421 E H I A R Y K V F S Y E E Y E E A F D E 480  
 ATAAAGGATATAATTTTATATGAGTCAGCCAACCTCAGGTGCTCTGGACGAAATGTTTAT  
 481 I K D I I S Y E S A N S G A L D E M F D 540  
 GTAAATACAAGAGTTGGTGAAACGTTTGACGAGTATTTTTTACAGCAAATGAGAATTGG  
 541 Y N T R V G E T F D E Y F L O O I E N W 600  
 CGCGAAAAGCTAGCTAAAGTCAATTAAAAATAACACCGAATTAGGTGAAGAGGACGTC  
 601 R E K L A K T A I K N N T E L G E E D V 660  
 AATTTTATTGTCAAAGACTATTAACAGAATTATTTTCTTAGAGTTTGTGAAGATAGA  
 661 N F I V O R L L N R I I F L R V C E D R 720  
 ACCATTGAAAAATATGAACAAATTAAGTATAAAAACTATGAGGAATTAAGATCTG  
 721 T I E K Y E T I K S I K N Y E E L K D L 780  
 TTTCAAAGTCTGATAGGAAATTTAATTCAGGTCTCTTTGACTTCATAGATGATACGCTC  
 781 F O K S D R K F N S G L F D F I D D T L 840  
 TTGCTTGAGGTTGAAATTGATTGCAATGATTGATAGAAATTTTAGTGATTATATTTT  
 841 L L E V E I D S N V L I E I F S D L Y F 900  
 CCACAAAGCCCATATGATTTTCTGTTGTCGATCCAACAATATTAAGCCAGATATATGAA  
 901 P O S P Y D F S V V D P T I L S O I Y E 960  
 CGTTTCTAGGTCAAGAAATAATTATAGAGTCAGGTGGTACATTTACATTACGGAGTCA  
 961 R F L G O E I I I E S G G T F H I T E S 1020

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FIG. 3C

2041 GAAAAGTATAATTCTGACCTTGGATATTTTATCTCCTGAAACAGAACTGTTTTTACT 2100  
 E K Y N S D P W I F L S P E T E A V F T  
 2101 AAATTTACAGAACTCAATTTGAGAACTTGGAGAAATCACTGATATAAGTGTAGGACTA 2160  
 K F T E A O F E K L G E I T D I S V G L  
 2161 CAAACAAGCGCTGATAAAATATATATTTTATTCCTGAAAATGAACTTCAGATACATAT 2220  
 O T S A D K I Y I F I P E N E T S D T Y  
 2221 ATATTTAATTATAAAGGAAAAGATATGAAATAGAAAATCTATATGTTGCCAGCTATC 2280  
 I F N Y K G K R Y E I E K S I C C P A I  
 2281 TATGACTTATCTTTTGGTCTTTTGAAGCATTGAGGAAATGCACAAATGATATTCCTT 2340  
 Y D L S F G S F E S I O G N A O M I F P  
 2341 TATGAAATCAGAGATGAAGAAGCATATCTACTAGAGGAAGAAACGCTTGAAAATGATTAT 2400  
 Y E I R D E E A Y L L E E E T L E N D Y  
 2401 CCTCTTGCTTGAATTATTTGAATGAGTTTAAAGAAGCTCTTGAAAAAGAAGCTTACAA 2460  
 P L A W N Y L N E F K E A L E K R S L O  
 2461 GGCCGTAATCCGAAATGGTATCAATATGGTGGTCCCAAAGTTTATCAAAATTCATGAT 2520  
 G R N P K W Y Q Y G R S O S L S K F H D  
 2521 AAAGAAAACTGATATGGACCGTACTGCTACGAAACCCCGTATGACTTGATAGGAAT 2580  
 K E K L I W T V L A T K P P Y V L D R N  
 2581 AACCTGTTATTTACTGGTGGTGAACCGACCGTATTATGGTTAATTAACCAATCTATT 2640  
 N L L F T G G G N G P Y Y G L I N O S I  
 2641 TACTCTTTGCATTATTTTATAGTATTCCTTCACATCCTGTAATAGAAAGTATGGTAAAA 2700  
 Y S L H Y F L G I L S H P V I E S H V K  
 2701 GCAAGGGCCAGTGAATTTAGGGATCATATTATCTCATGAAAACAATTTATTGAGAAA 2760  
 A R A S E F R G S Y Y S H G K O F I E K  
 2761 ATCCAATTAGAAAGATTGATTTTGATGATCAAGATGAGGTAGACAAATATAATACGGTG 2820  
 I P I R K I D F D O D E V D K Y N T V  
 2821 GTCACAACAGTAGAAAAATTAATTATAACTACCGATAGAAATAAAAGTGAGAGCAATGGA 2880  
 V T T V E K L I I T T D R I K S E S N G  
 2881 CCCCCGAGGAGAATGTTAAGAAGAAGGTAGATGCTTTGTCTAATCAACTTATCCAGGTT 2940  
 P R R R M L R R R L D A L S N O L I Q V  
 2941 ATTAATGAACTTTATAATATCAGTGACGAAGAATATACGACAGTTTGAATGATGAAATG 3000  
 I N E L Y N I S D E E Y T T V L N D E M  
 3001 TTGACAGCGCGTTAGGAGAAGAAAAATGA 3030  
 L T A A L G E E K \*

**FIG. 4**

